REMARKS

Amendments to the specification.

At the Examiner's request, the second paragraph at page 103 has been amended to comply with the Sequence Rules as specified in 37 CFR 1.822 (c).

Amendments to the claims.

Claims 22, 24, 27, 32 and 37 are currently amended. New claims 45-48 have been added. After this amendment, claims 22, 24-33, 36-38 and 41-48 will remain pending.

Allowability of claims 43 and 44.

The Examiner has determined that claims 43 and 44 are allowable. Applicants agree with this assessment, and thank the Examiner for his consideration.

Claims 22, 27, 32 and 37 as currently amended are directed to nucleic acid constructs, transgenic plants and methods to generate these plants that comprise a polynucleotide encoding an AT hook transcription factor polypeptide, wherein the polynucleotide hybridizes to of a nucleic acid sequence comprising SEQ ID NO: 13 or the complement thereof under stringent conditions that comprise 6X SSC at 65°C and two wash steps of 10 to 30 minutes with about 0.2x SSC, 0.1% SDS at 65°C or greater stringency, and wherein the polypeptide comprises a conserved domain that is at least 65% identical in amino acid sequence to amino acids 106-201 of SEQ ID NO: 14.

The previous Office action of August 20, 2008 cited Bevan's NCBI sequence Accession Number C71448, having an At-hook domain that is similar to that of instant SEQ ID NO: 14 and comprising a second conserved domain that is 71.9% identical to amino acids 106-201 of instant SEQ ID NO: 14. Applicants note that the claims 22, 24, and 26 are directed to recombinant constructs that comprise polynucleotides encoding AT hook transcription factors that are highly homologous to SEQ ID NO: 14. Bevan's NCBI reference only discloses the hypothetical, unannotated protein sequence (C71448) without any known utility, and does not teach one skill in the art to generate a recombinant construct comprising a polynucleotide to express the polypeptide C71448 or to transform a plant with the recombinant construct. Applicants note that a claim is anticipated only if each and every element of the claim is anticipated in a single art reference. Because Bevan's NCBI reference fails in teaching the recombinant construct claimed in the present invention, it should not be considered as an anticipatory prior art reference.

Regarding whether Bevan's NCBI reference in combination with Bevan et al. 1998 *Nature* publication that reports a 1.9Mb contiguous sequence from chromosome 4 of *Arabidopsis thanliana* has

rendered the claims 22, 24 or 26 obvious, Applicants note that the presently amended claim 24 is now limited to the recombinant constructs that comprise polynucleotides that can confer more drought tolerance or increased biomass relative to control plants when over-expressed in transgenic plants. Applicants note that obviousness can only be established by combining or modifying the teachings of the prior art to produce the claimed invention where there is some teaching, suggestion, or motivation to do so. *In re Kahn*, 441 F.3d 977, 986, 78 USPQ2d 1329, 1335 (Fed. Cir. 2006) (discussing rationale underlying the motivation-suggestion-teaching requirement as a guard against using hindsight in an obviousness analysis). The teaching, suggestion, or motivation must be found either explicitly or implicitly in the references themselves or in the knowledge generally available to one of ordinary skill in the art. Neither Bevan's C71448 nor Bevan's 1998 publication teaches any specific or significant utility for the polypeptide C71448; without any real world utility, one skilled artisan would not be motivated to combine these two references or modify the teachings of either to make a recombinant construct comprising a polynucleotide that encodes the polypeptide C71448 or to transform a plant with the recombinant construct. It is noted that Bevan's 1998 *Nature* publication (*Nature* Vol. 391, pages 485-872) discloses a 1.9 Mb contiguous region of Arabiodopsis chromosome 4, which includes at least 389 putative coding sequences and many other unmapped genes in this region of the genome (Figure 1 of Bevan et al., 1998 *Nature*). Bevan's *Nature* publication does not disclose the C71448 polypeptide or its coding sequence and should not be associated with the Bevan NCBI submission as a basis for an obvious rejection. (Applicants respectfully request the Examiner to advise where the C71448 is disclosed in Bevan's *Nature* publication if the Examiner disagrees with this statement). In KSR Int'l v. Teleflex Inc., 127 S. Ct. 1727, 1742 (2007), the Supreme Court noted that a claim is likely to be obvious "when there is a design need or market pressure to solve a problem and there are a finite number of identified, predictable solutions, a person of ordinary skill has good reason to pursue the known options within his or her technical grasp. If this leads to the anticipated success, it is likely the product not of innovation but of ordinary skill and common sense". In contrast, the NCBI reference discloses only a putative C71448 sequence without utility, and the *Nature* reference provides a laundry list of genes spanning over 1.9Mb of chromosomal DNA, which includes numerous non-characterized coding and non-coding sequences but not the coding sequence for C71448. In view of these disclosures, there is no good reason for a person of ordinary skill in the art to combine teachings the NCBI submission with the *Nature* publication and/or to pursue making recombinant constructs or transgenic plants comprising C71448.

It is also noted in MPEP 2145 that a conclusion of obviousness requires that the reference(s) relied upon be enabling in that it puts the public in possession of the claimed invention. In contrast, a person of

ordinary skill in the art, in view of Bevan's disclosures, would not be able to associate the polynucleotide encoding C71448 with the laundry list of unrelated genes disclosed in Bevan's *Nature* publication to generate a recombinant construct comprising the polynucleotide, and/or introduce it into a plant cell. The previous Office action stated that Bevan's *Nature* publication "using BAC clones which the instant art would recognize as being a recombinant construct as recited in the instant claims". Applicants respectfully disagree. As recognized by one of ordinary skill in the art, BAC clones are routinely used to contain large inserts (for example, inserts of 150-350 kbp, or greater than 700kbp) for genomic studies. However, BAC is not a vector of common choice to clone small molecules because purification and transformation of BAC clones are labor-intensive, inefficient and costly compared to other expression systems that are much more advantagrous in doing so; these expression vectors, such as those disclosed in Example II of the specification, can be readily obtained or modified to suit specific needs. Therefore, Bevan's disclosure of using BAC clone to analyze chromosome 4 of Arabidopsis does not enable one of ordinary skill in the art to generate recombinant constructs comprising the coding sequence of C71448, which is only 876bp. Furthermore, the Bevan *Nature* reference does not teach a BAC clone comprising the C71448-coding sequence, it spends enormous effort in describing findings of other 389 putative sequences instead. If one of ordinary skill in the art were to make a recombinant construct, he or she would pursue these 389 sequences instead of the C71448 sequence. Therefore, whether considered alone or in combination, Bevan's disclosures do not put the public in possession of the recombinant constructs or transgenic plants that overexpressing the C71448 peptides.

The Office action of August 20, 2008 states "It would have been *prima facie* obvious to one of ordinary skill in the art at the time of Applicant's invention that one would transform a plant cell with a recombinant construct encoding the taught polypeptide of Bevan et al 1998 in order to identify its function. In addition, one of ordinary skill in the instant art would have had a reasonable expectation of success in doing so. It is not necessary that the prior art suggest the combination to achieve the same advantage or result discovered by applicant." Applicants respectfully disagree and note that "[R]ejections on obviousness cannot be sustained by mere conclusory statements; instead, there must be some articulated reasoning with some rational underpinning to support the legal conclusion of obviousness." KSR, 550 U.S. 82 USPQ2d at 1396. MPEP 2141(III). The Office action fails in articulating the rationale why one of ordinary skill in the art would combine these two references. The Supreme Court in KSR has emphasized its focus on obviousness of combinations of known components: "A patent composed of several elements is not proved obvious merely by demonstrating that each element was independently known in the art" and "[t]he combination of familiar elements according to known methods is likely to be obvious when it does

no more than yield predictable results". (Id. at 1739), and "[w]hen a patent simply arranges old elements with each performing *the same function it had been known to perform*, and yields no more than one would expect from such an arrangement, the combination is obvious". Id. (quoting *Sakraida v. AG Pro, Inc.* 425 U.S. 273, 282 (1976), *emphasis* added). It has been established that when considering obviousness of a combination of known elements, the operative question is thus "whether the improvement is more than the predictable use of prior art elements according to their established functions." Recombinant constructs, plant cells or plants transformed with the polynucleotide encoding C71448 have never existed before the claimed invention. Neither Bevan's NCBI submission nor Bevan's *Nature* publication has predicted the instant results, or teaches a "function it had been known to perform", i.e. conferring increased biomass or more drought tolerance by C71448 overexpresson in plants. Thus, the skilled artisan would have been unable to predict the function of C71448, and the instant improvement is much more than the "predictable use of prior art elements" and it is not obvious to one of ordinary skill in the art to make a recombinant construct comprising a polynucleotide encoding C71448, and/or transform a plant cell with the construct, then test the plant for a useful function. Thus, the Bevan references do not render the claimed invention obvious.

In the Office action mailed on 7/9/2007, the Examiner cited Weigel et al., November 1999 (NCBI Accession No AAF07197). Applicants respectfully submit the relevant notebook records and the declaration by Dr. Cai-Zhong Jiang as attached (the unrelated portion has been blurred out), which show that Applicants conceived and considered the filing of a patent application of transgenic plants that overexpress the G1067 (SEQ ID NO: 4) sequence and methods for their generation no later than March 23, 1999, and introduced G1067 into plants on June 24, 1999. These activities occurred before the cited Weigel reference, November 1999 (NCBI Accession No AAF07197). Thus, the Weigel reference does not anticipate nor render the claimed invention obvious.

Response to specific items in the Office action.

Item 6. Rejection under 35 USC 112, first paragraph, written description

Applicants believe that the present rejection based on an alleged lack of written description has been avoided by the present amendment of the claims. Aspects of the rejection not addressed by the amendments to the claims are respectfully traversed.

The instant specification has provided a significant number of phylogenetically related AT hook transcription factors, including G3456 (SEQ ID NO:14), G3401 (SEQ ID NO:38), G3460 (SEQ ID NO:18), G2153 (SEQ ID NO:6), G3459 (SEQ ID NO:16), G1069 (SEQ ID NO:42), G1076 (SEQ ID

NO:54), G3556 (SEQ ID NO:40), G3399 (SEQ ID NO:10), G2157 (disclosed in Figure 12A, and also disclosed as SEQ ID NO: 448 in the priority US application No. 10/225,066), G3407 (SEQ ID NO:34), G1073 (SEQ ID NO:2), G3400 (SEQ ID NO:30), G1067 (SEQ ID NO:4), G2156 (SEQ ID NO:8), G1945 (SEQ ID NO:44), G3408 (SEQ ID NO:20). Each of these polypeptide sequences has a conserved AT hook motif and a second conserved domain that are highly homologous to amino acids 62-70 and 106-201 of G3456 SEQ ID NO: 14, respectively. The instant specification disclosed the amino acid coordinates of both domains in these polypeptide sequences (Table 1 and Figure 5A-5J). Applicants also have disclosed that the AT-hook domain of the disclosed sequences of sufficient homology to the AT-hook domain of G1073 (SEQ ID NO: 2) enable these polypeptides to bind the narrow minor groove of AT-rich regions of DNA and regulate transcription (page 25, lines 31-33). The specification has taught "the fragment or domain is a subsequence of the polypeptide that performs at least one biological function of the intact polypeptide in substantially the same manner, or to a similar extent, as does the intact polypeptide. For example, a polypeptide fragment can comprise a recognizable structural motif or functional domain such as a DNA-binding site or domain that binds a DNA promoter region and fragments can vary in size from as few as 3 amino acid residues to the full length of the intact polypeptide" (page 20, lines 12-19). The specification has also taught "more closely related transcription factors can share at least about 89% or about 100% identity in their AT-hook domains, and at least about 63%, or at least about 65% ...identity with the second conserved domain of G1073, (page 36). The second conserved domains, that are highly homologous to that of SEQ ID NO: 14, are present in all the functional sequences as disclosed in Table 1. Furthermore, Applicants have disclosed that a large number of sequences conferred increased drought tolerance or greater biomass when ectopically expressed in transgenic plants and all of these sequences have the common structural elements, i.e. conserved AT motifs and second conserved domains (also known as the DUF296 domain). These sequences include, for example, a majority of those listed in Table 1 of this response.

Table 1 Sequences that are phylogenetically-related to G3456 and their traits

GID	%ID in the sec. conserved domain to that of G3456	Seq ID	increased biomass	Drought tolerance	Species
G3456	100%	13/14	+[1]	+[2]	*Gm*
G3401	75%	37/38	+[6]	+[2]	*Os*
G3460	75%	17/18	+[1]	+[2]	*Gm*
G2153	74%	5/6	+[1]	+[2]	*At*
G3459	73%	15/16	+[1]	+[2]	*Gm*
G1069	71%	41/42	+[3]	+[4]	*At*
G1076	71%	53/54	N/T	N/T	*At*
G3556	69%	39/40	+[4]	+[3]	*Os*
G3399	68%	9/10	+[1]	+[3]	*Os*
G2157	66%	N/A	+[1]	+[3]	*At*
G3407	64%	33/34	+[1]	N/T*	*Os*
G1073	65%	1/2	+[1]	+[1]	*At*
G3400	63%	29/30	+[3]	+[3]	*Os*
G1067	61%	3/4	+[1]	+[1]	*At*
G2156	61%	7/8	+[3]	+[3]	*At*
G1945	51%	43/44	+[5]	+[5]	*At*
G3408	47%	19/20	+[3]	+[3]	*Os*

Gm: *Glycine max*, *Os: Oryza sativa*, *At: Arabidopsis thaliana*, NT: not fully tested.
+: transgenic plant lines ectopically expressing the sequence have the trait relative to controls
1: disclosed in the present application
2: disclosed in the declaration by Dr. Ratcliffe dated Jan 7th, 2008, submitted with previous amendment
3: disclosed in Table 36 of Application No. 60/961,403 (MBI-0065P)
4:disclosed in Table 11 of Application No. 60/713,952 (MBI-0061P)
5: disclosed in Table 5 of Application No. 11/981,733 (MBI-0091CIP)
6 disclosed in MBI-0068 CIP, 10/870,198

* plate-based dehydration assays did not show a positive water-deprivation tolerant phenotype, soil drought assays have not yet been performed

Applicants respectfully traverse the rejection and its supporting remarks. However, in order to facilitate prosecution in the present application Applicants have amended the claims without prejudice or disclaimer. Claims 22 and 27 do not include the functional limitation. One of ordinary skill in the art would clearly understand that the applicants had possession of the claimed invention based on Applicants' disclosure of the common structural elements that are related by the similar function retained among the claimed genus, and the numerous representative working examples.

The presently amended claims are directed to recombinant constructs, and transgenic plants comprising recombinant polynucleotides that can hybridize to SEQ ID NO: 13 under stringent conditions and also encode AT hook transcription factor polypeptides that comprise conserved domains that are at least 65% identical in amino acid sequence to amino acids 106-201 of SEQ ID NO: 14. Hybridization under stringent conditions requires a high degree of similarity in structure. "Because hybridization under highly stringent conditions requires a high degree of structural complementarity, nucleic acids that hybridize to the complement of SEQ ID NO: 1 must share many nucleotides in common with SEQ ID NO: 1. Thus, the claimed genus necessarily includes partial structures of SEQ ID NO: 1. The disclosure of SEQ ID NO: 1 combined with the knowledge in the art regarding hybridization would put one in possession of the genus of nucleic acids that would hybridize under stringent conditions to SEQ ID NO: 1" (Example 6 in USPTO written description guidelines, March 25, 2008). Applicants note that the claim 3 in Example 6 was rejected as failing to satisfy written description requirement because the specification discloses an actual reduction to practice of only one species of the claimed genus of nucleic acids (i.e. SEQ ID NO: 1). This is not the case with the present application where Applicants have disclosed numerous polynucleotides: G3456 (SEQ ID NO:13), G3401 (SEQ ID NO:37), G3460 (SEQ ID NO:17), G2153 (SEQ ID NO:5), G3459 (SEQ ID NO:15), G1069 (SEQ ID NO:41), G1076 (SEQ ID NO:53), G3556 (SEQ ID NO:39), G3399 (SEQ ID NO:9), G2157, G3407 (SEQ ID NO:33), G1073 (SEQ ID NO:1), G3400 (SEQ ID NO:29), G1067 (SEQ ID NO:3), G2156 (SEQ ID NO:7), G1945 (SEQ ID NO:43), G3408 (SEQ ID NO:19); these nucleotide sequences are predicted to hybridize to SEQ ID NO: 13 under stringent conditions of 0.2xSSC, 0.1%SDS at 65C (please see Exhibit A). These sequences, except G1076, which has not been fully tested, imparted drought tolerance and/or greater biomass when transformed into a plant (see Table 1 of this amendment). As described above, Applicants have also disclosed that these sequences share two conserved domains: the AT hook motif and the second conserved domain, which are definitively and putatively involved in DNA binding and transcription regulatory activity, respectively. The instant specification teaches "[a] conserved domain, with respect to presently disclosed AT-hook polypeptides refers to a domain within a transcription factor family that exhibits a higher degree of sequence homology, such as at least 62% sequence identity including conservative substitutions, and more preferably at least 65% sequence identity..." (page 14, lines 21-24 of the specification). Applicants have disclosed numerous examples, including those listed in Table 1 of this amendment, a majority of which, including G3456, G3401, G3460, G2153, G3459, G1069, G1076, G3556, G3399, G2157 and G1073, have at least 65% identical to G3456 in the second conserved domain (please see Exhibit C). All of these sequences except G1076, which has not been fully tested,

demonstrated the ability to impart enhanced drought tolerance and/or greater biomass when over-expressed in transgenic plants (please see Table 1 of this amendment). In addition, five G3456 homologous polypeptides are less similar to SEQ ID NO: 14 in the conserved domains that correspond to amino acids 106-201 of SEQ ID NO: 14 than instantly claimed peptides, and yet they conferred to plants greater drought tolerance or greater biomass relative to controls when over-expressed. These include rice sequences G3407 (64%), G3400 (63%) and G3408 (47%), arabidopsis sequences G1067 (61%), G2156 (61%) and G1945 (51%) (also listed in Table 1 of this amendment). These sequences are found in evolutionarily-distant plant species from both eudicots and monocots, such as *Arabidopsis* (G1067, G1069, G2157, G1073, G2156, G2153 and G1076), soy (G3459, G3460 and G3456), and rice (G3399, G3400, G3556, G3407, G3400, G3401 and G3556) and they represent a practical sampling of a large number of plant sequences. These working examples provide substantial evidence that the disclosed structure correlates with the claimed function. Regarding the USPTO's opinion on what constitutes a representative number when dealing with a genus of nucleotides, Applicants respectfully submit that the following statement is on point: "[w]hen there is substantial variation within the genus, it may require a description of the various species which reflect the variation within the genus. For example, a broadly drawn claim to a specific gene from ruminant mammals may require a representative species from cattle, buffalo, bison, goat, deer, antelope, camel, giraffe and llama" (Request for Comments on Interim Guidelines for Examination of Patent Applications Under the 35 U.S.C. 112 1 "Written Description" Requirement", 1212 OG 15, June 9, 1998). Note that there is no discussion of how the claims might be inadequately described because they may read on synthetic sequences. Applicants have provided functionally- and structurally-related polypeptide species that are representative of the claimed genus by having been derived from more evolutionarily diverse species (monocots and eudicots) than the mammals in the example provided by the USPTO. The variations within plant species from which the sequences are derived reflect the variations of the sequence species within the claimed genus, since the closer two plant species are in phylogeny, the more likely they will have structurally and functionally similar sequences. Therefore, Applicants have disclosed a representative number of sequences from diverse plant species, sufficient relevant identifying structure elements, i.e. the AT hook motif and the second conserved domain that are highly homologous to those present in G3456, SEQ ID NO: 14, and also functional characteristics, i.e. conferring drought tolerance or greater biomass, coupled with a disclosed correlation between the structure and function. In University of California v. Eli Lilly and Co., 119 F.3d 1559; 43USPQ2d1398, 1406(Fed. Cir. 1997), the court stated that "[a] description of a genus of cDNA may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence,

falling within the scope of the genus or of a recitation of structural features common to members of the genus, which features constitute a substantial portion of the genus." Since a significant number of these sequences are phylogenetically and sequentially related to each other and have been shown to increase a plant's biomass, and/or drought tolerance, one skilled in the art would predict that other similar, phylogenetically related sequences falling within the present clades of transcription factors would also perform similar functions when ectopically expressed. Thus, those of ordinary skill in the art would recognize that Applicants are in possession of the large number of the functional plant sequences that are able to hybridize to the SEQ ID NO: 13 and or the complement thereof and encode AT transcription factor polypeptides that are at least 65% identical in amino acid sequence to amino acids 106-201 of G3456 (SEQ ID NO: 14).

The newly added claims 45-48, which depend on claims 22, 27, 32 and 37 respectively, are further limited in that the polypeptide encoded by the polynucleotide comprised in the recombinant construct also shares at least 60% sequence identity to SEQ ID NO: 14. Applicants have disclosed a soy sequence G3456 (SEQ ID NO: 14), two *Arabidopsis* sequences G1069 (SEQ ID NO: 42) and G2153 (SEQ ID NO: 6) and a rice sequence G3401 (SEQ ID NO: 38); these sequence share 100%, 60.4%, 66.1% and 61.5% sequence identity with SEQ ID NO: 14, respectively (please see Exhibit B). The specification has shown that transgenic plants transformed with G2153 or G3456 had increased biomass (page 60, lines 6-9 and page 92, lines 24-26, page 95, line 6). Applicant's patent application 10/870,198 (e.g., on page 60, lines 23 of the 10/870,198 specification, filed 6/16/2004) shows that G3401can be used to make larger plants. U.S. patent application 12/077,535, filed 03-17-2008, also shows that G3401 can confer increased biomass (page 167, the "G3401", rows showing "More tol. to drought* and better recovery from drought treatment" and "Larger leaf size"). G3456, G2153 and G3401 have been shown to confer drought tolerance in the previously-submitted declaration by Dr. Ratcliffe. G1069 has been shown to confer increased biomass in plants (row "G1069" of Table 36 of Applicant's application 60/961,403) and increased abiotic stress tolerance (the row containing "G1069" of Table 36 of Applicant's application 60/961,403). The abiotic stress tolerance may include salt, hyperosmotic stress, heat, cold, drought, or low nitrogen conditions.(Page 4, lines 22-23 of application 60/961,403). The Office action states that "Applicants' evidence of polypeptide sequence identity appears to be directed to species at the extremes of the claimed genus, and do not describe the variation within the genus". Applicants respectfully and fervently disagree with this assessment. Applicants have disclosed four variants within the genus, G1069 (60.4% identity to SEQ ID NO: 14), G3401 (61.5% identity to SEQ ID NO: 14), G2153 (66.5% identity to SEQ ID NO: 14) and G3456 (100% identity to SEQ ID NO: 14), which can impart greater biomass or

drought tolerance to transgenic plants when overexpressed. Applicants have also disclosed the conserved structure elements, i.e. the AT motif and the second conserved domain, coupled with the function of conferring drought tolerance or greater biomass. One of ordinary skill in the art would recognize that sequences that have higher similarity in structure, i.e. higher than 66.5% to SEQ ID NO: 14 would more likely have similar functions to that of SEQ ID NO: 14. Sequences with higher homology for example, 80% or 90% or even greater sequence identity to G3456 could be readily made available through conserved amino acid substitutions or similar amino acid substitutions, for example, those listed in Table 3 or Table 4 of the specification, outside the AT motif and the second conserved domain, and they would have the similar function to G3456. These disclosed polypeptide sequences having the described structure and function are derived from very diverse species, including rice, soy and *Arabidopsis* and they represent a practical sampling of considerably large number of plant sequence species from both eudicot and monocot plants. For example, between the monocot plant rice and eudicot plant soy, there are a large number of dicot species that could generate sequences more closely related to soy G3456 than to rice G3401, i.e. sequences that have an amino acid sequence identity of greater than 61.5% to G3456 (SEQ ID NO: 14) and have the function of conferring greater tolerance to drought and improving the biomass of a plant when over-expressed. It is noted that Applicants are not required to exemplify each and every claimed embodiment of his or her invention. Rather, "if a person of ordinary skill in the art would have understood the inventor to have been in possession of the claimed invention at the time of filing, even if every nuance of the claims is not explicitly described in the specification, then adequate written description requirement is met" (*In re Alton*, 37 USPQ2d 1578, 1584 (Fed. Cir. 1996)). Thus one of ordinary skill in the art would recognize that at the filing time, Applicants were in possession of the sequences that hybridize to SEQ ID NO: 13 and encode the polypeptides having at least 60% amino acid sequence identity to SEQ ID NO:14.

Accordingly, Applicants respectfully request that the present rejection under 35 USC 112, first paragraph, for lack of written description, be withdrawn.

Item 7. Rejection under 35 USC 112, first paragraph, enablement

The Office action rejected claims 22 and 24-31 under 35 USC112, first paragraph, for lack of enablement. In particular, the Office action acknowledges that the claims are enabled for claims regarding a recombinant construct comprising a polynucleotide encoding SEQ ID NO: 14 and methods of using same, but asserted that enablement has not been provided for all sequences are at least 60% identical to

SEQ ID NO: 14 and methods of using same. This rejection and its supporting remarks are respectfully traversed for the reasons set forth below.

As described above, Applicants have provided numerous examples of polynucleotide sequences that can hybridize to SEQ ID NO: 13 or the complement thereof under stringent conditions and/or encode polypeptides that have the AT hook motif and the second conserved domain that are at least 65% identical to 106-201 of SEQ ID NO: 14, and/or encode polypeptides that share at least 60% sequence identity to SEQ ID NO: 14. The AT hook motif is art known as a DNA binding motif. The second conserved domain, referred to as a domain with unknown function (page 27), comprises a significant majority of the art-recognized DUF296 domain by conserved domain analysis using methods provided at www.ncbi.nlm.nih.gov. Alves et al., 2009 also noted that DUF296 is a domain of unknown function that contains what appears to be a zinc finger like motif, which suggests that these proteins may be involved in DNA binding, probably acting in regulation of gene expression (the second paragraph at page 10 of Alves et al., 2009). Richardt et al., 2007 also recognized that "PT007 might represent a novel TF family is fortified by the domain structure of the members, most of which contain the two PFAM domains AT hook (PF02178) ... and DUF296 (PF03479), which are known to be present in this particular order in a class of proteins that is thought to have DNA-binding activity" (column 2, page 1459 of Richardt et al., 2007). Richardt also cited Weigel et al., 2000 in which overexpression of a protein containing DUF296 has been shown to lead to late flowering and modified leaf development in Arabidopsis (column 2, page 1459 of Richardt et al., 2007). Thus, applicants have provided the conserved structure elements of the claimed genus of sequences. The fully tested polynucleotides conferred drought tolerance and/or greater biomass when overexpressed in a transgenic plant. These sequences represent a practical sampling of a large number of sequence species. Through these numerous examplar plant sequence species, Applicants have demonstrated the correlation between the common structure elements and the conserved function. Applicants have found that a wide variety of plant species have orthologous or closely-related homologous sequences that function as does G3456; the numerous claimed G3456 homologs derived from both eudicots and monocots that have been introduced into plants have been shown to confer greater tolerance to drought or greater biomass relative to control plants when the sequences were overexpressed. These studies suggested that numerous genes from diverse plant species are likely to function similarly (i.e., by regulating similar target sequences and controlling the same traits) and thus finding and using sequences that function similarly would not require undue effort..

Furthermore, considering the high degree of correlation between the claimed structure and function, there is no need to modify a claimed sequence species. If one wished to do so, testing methods

are disclosed and routine. It is well within the level of skill of the average artisan to test the modifications in plants, and guidance for making conservative substitutions is art-known and provided (e.g., with DNASTAR software, see page 18, lines 19-24 of the specification). Applicants believe their concrete guidance in the form of working examples address a number of the Examiner's concerns, and weigh in favor of the specification enabling one skilled in the art to make and use the claimed plants. Assuming that sufficient reason for such doubt could exist, which Applicants dispute, such a rejection can be overcome by suitable proofs indicating that the teaching contained in the specification is truly enabling (*In re Marzocchi*, 439 F.2d 220, 223, 169 USPQ 367, 369 (CCPA 1971); original *emphasis*). Applicants believe suitable proofs in the form of a one-to-one correlation with structure and function and the breath of the working examples indicates that the teaching contained in the specification is truly enabling.

The specification has taught in detail how to identify additional sequences by hybridization method and percentage identity, how to transform plants, identify the transformants and test them for greater biomass or drought tolerance (see Examples I-VIII). The fact that some experimentation is necessary does not preclude enablement; what is required is that the amount of experimentation must not be unduly extensive. In Atlas Powder Co. v. E.I. DuPont de Nemours & Co., 750 F.2d 1569, 1576, 224 USPQ 409, 413 (Fed. Cir. 1984), the Patent and Trademark Office Board of Appeals stated: "The test is not merely quantitative, since considerable amount of experimentation is permissible, if it is merely routine, or if the specification in question provides a reasonable amount of guidance with respect to the direction in which the experimentation should proceed to enable the determination of how to practice a desired embodiment of the invention claimed". It is also well established that routine experimentation may be warranted to determine whether use of a thing or a method is or is not within the scope of a claim, and does not negate the patentability of the claim (In re Wands, 858F.2d 731, 8 USPQ2d 1400 (Fed. Cir. 1988)). Given the disclosure of the conserved structure elements i.e. the AT motif and the second conserved domain and related functional characteristics present in numerous phylogenetically diverse plant species, the detailed guidance of how to identify sequences of the disclosed structure and function through hybridization and percent identity, and the knowledge in the art at the time of filing, it would at most require routine experimentation to obtain other sequences encoding polypeptides having more than 60% sequence identity to SEQ ID NO: 14, or having more than 65% sequence identity to amino acid 106-201 of SEQ ID NO: 14. Thus, Applicants believe that the full scope of currently claimed subject matter is enabled.

Accordingly, Applicants respectfully request that the rejection under 35 USC 112, first paragraph, for lack of enablement, be withdrawn.

CONCLUSION

Applicants believe that no additional fee is due with this communication. However, if the USPTO determines that a fee is due, the Commissioner is hereby authorized to charge Mendel Biotechnology, Inc. Deposit Account No. **50-1025.**

Respectfully submitted,
MENDEL BIOTECHNOLOGY, INC.

Date: July 22, 2009

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Notebook pages of Cai-Zhong Jiang and Andrew Mason
Reference of Alves et al., 2009,
Reference of Richardt et al., 2007

Exhibit A. Polynucleotide subsequences used for hybridization analysis

The best identity match of 50-base subsequences from G3456 and homolog DNAs are listed below and were used for determining theoretical melting temperatures. The first sequence in each pair is the 50 base subsequence derived from G3456, and the second sequence of each pair is the reverse complement of the corresponding subsequence from each optimally-aligned G3456 homolog. The T_m(conc) (the point at which the concentration of double-stranded molecules of one-half of its maximum value defines the melting temperature) was used to determine theoretical melting temperatures at 0.2x SSC (about 30 mM Na^+). Determinations made with DINAMelt server available at: www.bioinfo.rpi.edu/applications/hybrid/hybrid2.php.

```
G3456    CCCTGGGCCGTCCCCTCCCGGCGCCACCGGGCTCACAATCTACCTCGCCG
G3456    CGGCGAGGTAGATTGTGAGCCCGGTGGCGCCGGGAGGGGACGGCCCAGGG
Tm(conc) 0.2x SSC: 82.3° C

G3456    CCTCGCCGGAGGCCAGGGGCAGATCGTCGGCGGCGAAGTGGTGGGCCCAC
G3399    GCGGGCCCACCACGCTGCCGCCGATCACCTGGCCCTGGCCGCCGGAGAGG
Tm(conc) 0.2x SSC: 75.5° C

G3456    CGCCCTAGGGGACGTCCACCGGGCTCCAGAAACAAGCCGAAACCGCCGAT
G1067    ATCGGTGGCTTGGCTTTGTTCTTAGATCCTGGTGGACGTCCACGTGGACG
Tm(conc) 0.2x SSC: 69.1° C

G3456    GAGACAGCCCCAACGCACTCCGTAGCCATGTCTTGGAGATCTCCGACGGC
G1069    TCCGACGGCAATCTCCATGACGTGGCTCCGCAGCGCGTTAGGGCTGTCTC
Tm(conc) 0.2x SSC: 69.8° C

G3456    CCTCCCGGCGCCACCGGGCTCACAATCTACCTCGCCGGAGGCCAGGGGCAG
G3400    CTGGCCCTGCCCGCCGGAGAGGAAGACGGTGAGGCCGCTGGCGCTGGGCGG
Tm(conc) 0.2x SSC: 76.7° C

G3456    CCTCCCGGCGCCACCGGGCTCACAATCTACCTCGCCGGAGGCCAGGGGCA
G3556    TGCCCCTGCCCGCCGGCGAGGTACACGGCGAGCCCCGTGGCCCCTGGCGG
Tm(conc) 0.2x SSC: 77.6° C

G3456    GTCACCCGAGACAGCCCTAACGCGCTGCGGAGCCACGTCATGGAGATTGC
G2157    GCAATCTCAAGAACATGGCTCTGGAGAGAGTTAGGGCTTTCTTTGGTAAC
Tm(conc) 0.2x SSC: 68.7° C
```

G3456 CTCGCCGGAGGCCAGGGGCAGATCGTCGGCGGCGAAGTGGTGGGCCCACT
G3408 AGCGGGCCTGCCACGGCCCCGCCGACGATCTGGCCGTGCGGGCCGGCGAG
T_m (conc) 0.2x SSC: 79.8° C

G3456 CGCCGCCCTAGGGGACGTCCACCGGGCTCCAGAAACAAGCCGAAACCGCC
G3407 GGCGGCTTGGGCTTGTTCTTGGAGCCCGGCGGGCGGCCGCGGGGGCGGCG
T_m (conc) 0.2x SSC: 74.8° C

G3456 AGCGGCAGCGGGACCGTCGTCAACGTCAATCTCCGGCAACCCACGGCACC
G1073 GGAGCCGCAGGTTGCCGTATCGTGACGTTAGTGACCGCACCCGTGCCGCT
T_m (conc) 0.2x SSC: 70.2° C

G3456 CGCCCTAGGGGACGTCCACCGGGCTCCAGAAACAAGCCGAAACCGCCGAT
G2156 ACCGGTGGCTTCGGCTTGTTCTTGGATCCCGGAGGACGTCCACGTGGACG
T_m (conc) 0.2x SSC: 71.8° C

G3456 CCTCCCGGCGCCACCGGGCTCACAATCTACCTCGCCGGAGGCCAGGGGCA
G3400 TGGCCCTGCCCGCCGGAGAGGAAGACGGTGAGGCCGCTGGCGCTGGGCGG
T_m (conc) 0.2x SSC: 76.8° C

G3456 CGCCCTAGGGGACGTCCACCGGGCTCCAGAAACAAGCCGAAACCGCCGAT
G2156 ACCGGTGGCTTCGGCTTGTTCTTGGATCCCGGAGGACGTCCACGTGGACG
T_m (conc) 0.2x SSC: 71.8° C

G3456 CCACCGGGCTCCAGAAACAAGCCGAAACCGCCGATATTCGTCACCCGAGA
G1076 TCGCGCGTGATAATTACCGGAGGTTTCGGTTTGTTCTTGGATCCCGGTGG
T_m (conc) 0.2x SSC: 69.4° C

G3456 CGCCGCCCTAGGGGACGTCCACCGGGCTCCAGAAACAAGCCGAAACCGCC
G1945 GGTGGTTTAGGTTTGTTTTTGGAACCTGGTGGTCTGCCACGTGGACGTCG
T_m (conc) 0.2x SSC: 69.4° C

G3456 GCCACCGGGCTCACAATCTACCTCGCCGGAGGCCAGGGGCAGATCGTCGG
G3460 CCGACGACCTGGCCCTGCCCGCCGGCGAGGTAGATTGTGAGACTGGTGGC
T_m(conc) 0.2x SSC: 72.0° C

G3456 GCCACCGGGCTCACAATCTACCTCGCCGGAGGCCAGGGGCAGATCGTCGG
G3459 CCGACAACCTGCCCCTGCCCGCCGGCCAGGTAGATTGTGAGGCTGGTGGC
T_m(conc) 0.2x SSC: 71.8° C

G3456 GTCACCCGAGACAGCCCTAACGCGCTGCGGAGCCACGTCATGGAGATTGC
G2153 GCGATCTCCATGACATGGCTCTTGAGAGCATTTGGAGAATCGCGAGTGAC
T_m(conc) 0.2x SSC: 70.0° C

G3456 CCTCCCGGCGCCACCGGGCTCACAATCTACCTCGCCGGAGGCCAGGGGCA
G3401 TGCCCCTGCCCGCCGGCGAGGTACACGGTCAGCCCGGTGGAGCCCGGCGG
T_m(conc) 0.2x SSC: 77.2° C

Exhibit B Comparison of the full length sequence of G3456 and its homologs by Accelrys Gene2.5

Pairwise Matrix: GONNET
Align Speed: Slow
Open Gap Penalty: 10.000
Extended Gap Penalty: .100

Multiple Matrix: GONNET
Mulitple Open Gap Penalty: 10.000
Multiple Extended Gap Penalty: .05
Delay Divergent: 30

Gap Separation Distance: 8
End Gap Separation: false
Residue Specific Penalties: false
Hydrophilic Penalties: false
Hydrophilic Residues: GPSNDQEKR

Alignment Score 896

Percent Identity Matrix

	G3456	G3401
G3456	100.0	61.5
G3401	61.5	100.0

Pairwise Matrix: GONNET
Align Speed: Slow
Open Gap Penalty: 10.000
Extended Gap Penalty: .100

Multiple Matrix: GONNET
Mulitple Open Gap Penalty: 10.000
Multiple Extended Gap Penalty: .05
Delay Divergent: 30

Gap Separation Distance: 8
End Gap Separation: false
Residue Specific Penalties: false
Hydrophilic Penalties: false
Hydrophilic Residues: GPSNDQEKR

Alignment Score 1048

Percent Identity Matrix

	G3456	G2153
G3456	100.0	66.1
G2153	66.1	100.0

Pairwise Matrix: GONNET
Align Speed: Slow
Open Gap Penalty: 10.000
Extended Gap Penalty: .100

Multiple Matrix: GONNET
Mulitple Open Gap Penalty: 10.000
Multiple Extended Gap Penalty: .05
Delay Divergent: 30

Gap Separation Distance: 8
End Gap Separation: false
Residue Specific Penalties: false
Hydrophilic Penalties: false
Hydrophilic Residues: GPSNDQEKR

Alignment Score 998

Percent Identity Matrix

	G3456	G1069
G3456	100.0	60.4
G1069	60.4	100.0

Exhibit C Comparison of the second conserved domain of G3456 and its homologs

G3401

```
 Identities = 72/96 (75%)

G3456:   VAQFARRRQRGVSILSGSGTVVNVNLRQPTAPGAVMALHGRFDILSLTGSFLPGPSPPGA
         +A FARRRQRGV +LSG+GTV +V LRQP AP AV+AL GRF+ILSLTG+FLPGP+PPG+
G3401:   IAHFARRRQRGVCVLSGAGTVTDVALRQPAAPSAVVALRGRFEILSLTGTFLPGPAPPGS

G3456:   TGLTIYLAGGQGQIVGGEVVGPLVAAGPVLVMAATF
         TGLT+YLAGGQGQ+VGG VVG L AAGPV+V+A+TF
G3401:   TGLTVYLAGGQGQVVGGSVVGTLTAAGPVMVIASTF
```

G3460

```
 Identities = 72/96 (75%)

G3456:   VAQFARRRQRGVSILSGSGTVVNVNLRQPTAPGAVMALHGRFDILSLTGSFLPGPSPPGA
         V  +ARRRQRG+ +LSGSGTV NV+LRQP A GAV+ LHGRF+ILSL+GSFLP P+PPGA
G3460:   VTAYARRRQRGICVLSGSGTVTNVSLRQPAAAGAVVRLHGRFEILSLSGSFLPPPAPPGA

G3456:   TGLTIYLAGGQGQIVGGEVVGPLVAAGPVLVMAATF
         T LTIYLAGGQGQ+VGG VVG L AAGPV+V+AA+F
Sbjct:   TSLTIYLAGGQGQVVGGNVVGELTAAGPVIVIAASF
```

G2153

```
 Identities = 77/104 (74%)

G3456:   VAQFARRRQRGVSILSGSGTVVNVNLRQPT------APG--AVMALHGRFDILSLTGSFL
         +A FARRRQRG+ ILSG+GTV NV LRQP+       APG  AV+AL GRF+ILSLTGSFL
G2153:   LATFARRRQRGICILSGNGTVANVTLRQPSTAAVAAAPGGAAVLALQGRFEILSLTGSFL

G3456:   PGPSPPGATGLTIYLAGGQGQIVGGEVVGPLVAAGPVLVMAATF
         PGP+PPG+TGLTIYLAGGQGQ+VGG VVGPL+AAGPV+++AATF
Sbjct:   PGPAPPGSTGLTIYLAGGQGQVVGGSVVGPLMAAGPVMLIAATF
```

G3459

```
 Identities = 71/96 (73%)

G3456:   VAQFARRRQRGVSILSGSGTVVNVNLRQPTAPGAVMALHGRFDILSLTGSFLPGPSPPGA
         V  +ARRRQRG+ +LSGSGTV NV+LRQP A GAV+ LHGRF+ILSL+GSFLP P+PPGA
G3459:   VTAYARRRQRGICVLSGSGTVTNVSLRQPAAAGAVVTLHGRFEILSLSGSFLPPPAPPGA

G3456:   TGLTIYLAGGQGQIVGGEVVGPLVAAGPVLVMAATF
         T LTIYLAGGQGQ+VGG V+G L AAGPV+V+AA+F
G3459:   TSLTIYLAGGQGQVVGGNVIGELTAAGPVIVIAASF
```

G1069

```
 Identities = 69/96 (71%)

G3456:.  VAQFARRRQRGVSILSGSGTVVNVNLRQPTAPGAVMALHGRFDILSLTGSFLPGPSPPGA
         +A F+RRRQRGV +LSG+G+V NV LRQ  APG V++L GRF+ILSLTG+FLPGPSPPG+
G1069:   IAHFSRRRQRGVCVLSGTGSVANVTLRQAAAPGGVVSLQGRFEILSLTGAFLPGPSPPGS
```

```
G3456:   TGLTIYLAGGQGQIVGGEVVGPLVAAGPVLVMAATF
         TGLT+YLAG QGQ+VGG VVGPL+A G V+V+AATF
G1069:   TGLTVYLAGVQGQVVGGSVVGPLLAIGSVMVIAATF
```

G1076

```
 Identities = 69/96 (71%)

G3456:   VAQFARRRQRGVSILSGSGTVVNVNLRQPTAPGAVMALHGRFDILSLTGSFLPGPSPPGA
         VA +ARRRQRG+ +LSGSGTV NV++RQP+A GAV+ L G F+ILSL+GSFLP P+PPGA
G1076:   VATYARRRQRGICVLSGSGTVTNVSIRQPSAAGAVVTLQGTFEILSLSGSFLPPPAPPGA

G3456:   TGLTIYLAGGQGQIVGGEVVGPLVAAGPVLVMAATF
         T LTI+LAGGQGQ+VGG VVG L AAGPV+V+AA+F
G1076:   TSLTIFLAGGQGQVVGGSVVGELTAAGPVIVIAASF
```

G3556

```
 Identities = 67/97 (69%)

G3456:   VAQFARRRQRGVSILSGSGTVVNVNLRQPTAPGAV-MALHGRFDILSLTGSFLPGPSPPG
         +A F+RRRQRGVS+LSGSG V NV LRQP   GA  +AL GRF+ILS++G+FLP P+PPG
G3556:   IAGFSRRRQRGVSVLSGSGAVTNVTLRQPAGTGAAAVALRGRFEILSMSGAFLPAPAPPG

G3456:   ATGLTIYLAGGQGQIVGGEVVGPLVAAGPVLVMAATF
         ATGL +YLAGGQGQ+VGG V+G L+A+GPV+V+AATF
G3556:   ATGLAVYLAGGQGQVVGGSVMGELIASGPVMVIAATF
```

G3399

```
 Identities = 68/99 (68%)

G3456:   VAQFARRRQRGVSILSGSGTVVNVNLRQPTA--PGAVMA-LHGRFDILSLTGSFLPGPSP
         VA++ARRR RGV +LSG G VVNV LRQP A  PG+++A L GRF+ILSLTG+ LP P+P
G3399:   VAEYARRRGRGVCVLSGGGAVVNVALRQPGASPPGSMVATLRGRFEILSLTGTVLPPPAP

G3456:   PGATGLTIYLAGGQGQIVGGEVVGPLVAAGPVLVMAATF
         PGA+GLT++L+GGQGQ++GG VVGPLVAAGPV++MAA+F
G3399:   PGASGLTVFLSGGQGQVIGGSVVGPLVAAGPVVLMAASF
```

G2157

```
 Identities = 64/96 (66%)

G3456:   VAQFARRRQRGVSILSGSGTVVNVNLRQPTAPGAVMALHGRFDILSLTGSFLP-GPSPPGATG
            FARRR RGVS+LSGSG V NV LRQP A G V++L G+F+ILS+ G+FLP   SP  A G
G2157:   LNAFARRRGRGVSVLSGSGLVTNVTLRQPAASGGVVSLRGQFEILSMCGAFLPTSGSPAAAAG

G3456:   LTIYLAGGQGQIVGGEVVGPLVAAGPVLVMAATF
         LTIYLAG QGQ+VGG V GPL+A+GPV+V+AATF
G2157:   LTIYLAGAQGQVVGGGVAGPLIASGPVIVIAATF
```

G3407

```
 Identities = 66/102 (64%)

G3456:   VAQFARRRQRGVSILSGSGTVVNVNLRQPTA--PG----AVMALHGRFDILSLTGSFLPGPSP
            +ARRRQRGV +LS +GTV NV LRQP +  PG    AV  LHGRF+ILSL GSFLP P+P
G3407:   LTAYARRRQRGVCVLSAAGTVANVTLRQPQSAQPGPASPAVATLHGRFEILSLAGSFLPPPAP

G3456:   PGATGLTIYLAGGQGQIVGGEVVGPLVAAGPVLVMAATF
         PGAT L  +LAGGQGQ+VGG V G L+AAGPV+V+AA+F
G3407:   PGATSLAAFLAGGQGQVVGGSVAGALIAAGPVVVVAASF
```

G1073

```
 Identities = 64/98 (65%)

G3456:   VAQFARRRQRGVSILSGSGTVVNVNLRQPTAP--GAVMALHGRFDILSLTGSFLPGPSPP
         V+ +A RR  GV I+SG+G V NV +RQP AP  G V+ LHGRFDILSLTG+ LP P+PP
G1073:   VSTYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGRFDILSLTGTALPPPAPP

G3456:   GATGLTIYLAGGQGQIVGGEVVGPLVAAGPVLVMAATF
         GA GLT+YLAGGQGQ+VGG V G L+A+GPV++MAA+F
G1073:   GAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASF
```

G3400

```
 Identities = 63/99 (63%)

G3456:   VAQFARRRQRGVSILSGSGTVVNVNLRQPTA--PGAVMA-LHGRFDILSLTGSFLPGPSP
         V +FARRR RGVS+LSG G V NV LRQP A  PG+++A + G+F+ILSLTG+ LP P+P
G3400:   VCEFARRRGRGVSVLSGGGAVANVALRQPGASPPGSLVATMRGQFEILSLTGTVLPPPAP

G3456:   PGATGLTIYLAGGQGQIVGGEVVGPLVAAGPVLVMAATF
         P A+GLT++L+GGQGQ+VGG V G L+AAGPV +MAA+F
G3400:   PSASGLTVFLSGGQGQVVGGSVAGQLIAAGPVFLMAASF
```

G1067

```
 Identities = 65/105 (61%)

G3456:   VAQFARRRQRGVSILSGSGTVVNVNLRQPTAPG---------AVMALHGRFDILSLTGSF
         V+ +ARRR RGVS+L G+GTV NV LRQP  PG           V+ LHGRF+ILSLTG+
G1067:   VSTYARRRGRGVSVLGGNGTVSNVTLRQPVTPGNGGGVSGGGGVVTLHGRFEILSLTGTV

G3456:   LPGPSPPGATGLTIYLAGGQGQIVGGEVVGPLVAAGPVLVMAATF
         LP P+PPGA GL+I+LAGGQGQ+VGG VV PL+A+ PV++MAA+F
G1067:   LPPPAPPGAGGLSIFLAGGQGQVVGGSVVAPLIASAPVILMAASF
```

G2156

```
 Identities = 65/105 (61%)

G3456:   VAQFARRRQRGVSILSGSGTVVNVNLRQPTAP---------GAVMALHGRFDILSLTGSF
         V  +ARRR RGVSILSG+GTV NV+LRQP             G V+ALHGRF+ILSLTG+
G2156:   VTTYARRRGRGVSILSGNGTVANVSLRQPATTAAHGANGGTGGVVALHGRFEILSLTGTV

G3456:   LPGPSPPGATGLTIYLAGGQGQIVGGEVVGPLVAAGPVLVMAATF
         LP P+PPG+ GL+I+L+G QGQ++GG VV PLVA+GPV++MAA+F
G2156:   LPPPAPPGSGGLSIFLSGVQGQVIGGNVVAPLVASGPVILMAASF
```

G1945

```
 Identities = 53/103 (51%)

G3456:   VAQFARRRQRGVSILSGSGTVVNVNLRQPT--APGAVMALHGRFDILSLTGSFLPGP---
         + +F RR+  GV +LSGSG+V NV LRQP+  A G+ +  HG+FD+LS++ +FLP P
G1945:   INRFCRRKSIGVCVLSGSGSVANVTLRQPSPAALGSTITFHGKFDLLSVSATFLPPPPRT

G3456:   --SPPGATGLTIYLAGGQGQIVGGEVVGPLVAAGPVLVMAATF
           SPP +   T+ LAG QGQI+GG V GPL++AG V V+AA+F
G1945:   SLSPPVSNFFTVSLAGPQGQIIGGFVAGPLISAGTVYVIAASF
```

G3408

```
 Identities = 51/108 (47%)

G3456:   VAQFARRRQRGVSILSGSGTVVNVNLRQPT--APG---AVMALHGRFDILSLTGSFLPGP
         +A+F+ RR  G+ +L+G+G V NV+LR P+   PG   A +  HGR++ILSL+ +FLP
G3408:   LARFSSRRNLGICVLAGTGAVANVSLRHPSPGVPGSAPAAIVFHGRYEILSLSATFLPPA

G3456:   -------SPPGATGLTIYLAGGQGQIVGGEVVGPLVAAGPVLVMAATF
                 +   A GL+I LAG  GQIVGG V GPL AA  V+V+AA F
G3408:   MSSVAPQAAVAAAGLSISLAGPHGQIVGGAVAGPLYAATTVVVVAAAF
```